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① This does not appear to be
in ASCII text

② No "General Information" has
been included, which is mandatory.
Please see attached sample
of what the Sequence Listing should
look like.

Patent Application US/07/728,838

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119 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG è
120 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTTè
121 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTCGA AGTTCCGCCT ACAGCTCTAGè
122 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTCè
123 CCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTATè
124 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGTè
125 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCTè
126 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CCè
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148 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
149 5 10 15
150 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAAè
151 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
152 20 25 30
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154 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
155 35 40 45
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157 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
158 50 55 60
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166	Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp	
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169	Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu	
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187	Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro	
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212	GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT	60

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265 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT â

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370 ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA @
371 AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA @

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372 GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC ê
373 TTC TCA CCT TAG ê
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375 GCTAAGAGCA TCTTTTTTAAA AAATATTATT GGTAAGCTAA ACAATTGTGA ê
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396 GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA ê
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419 Leu Leu His Arg Tyr Ser Leu Glu Glu Ile Leu Pro Tyr Leu Gly Trp
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447 GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC ê

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474 CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT ê

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477 CTGAGCATGA GTTGACAGCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC ê

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126	Unknown or Misplaced Identifier	TATCTTAAC	TAGCTCGGCT TCCTGCTGGT ACCCTTT
127	Unknown or Misplaced Identifier	T	
128	Unknown or Misplaced Identifier	(2)A	
130	Unknown or Misplaced Identifier	A	
132	Unknown or Misplaced Identifier	A	
135	Unknown or Misplaced Identifier	A	
138	Unknown or Misplaced Identifier	A	
141	Unknown or Misplaced Identifier	A	
143	Unknown or Misplaced Identifier	A	

LINE ERROR

ORIGINAL TEXT

147	Unknown or Misplaced Identifier	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC	
148	Unknown or Misplaced Identifier	Met Ser Asp Asn Lys Lys Pro Asp Lys Ala	
149	Unknown or Misplaced Identifier	5	10 1
150	Unknown or Misplaced Identifier	GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG	
151	Unknown or Misplaced Identifier	Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu	
152	Unknown or Misplaced Identifier	20	25
153	Unknown or Misplaced Identifier	GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	
154	Unknown or Misplaced Identifier	Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val	
155	Unknown or Misplaced Identifier	35	40
156	Unknown or Misplaced Identifier	AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC	
157	Unknown or Misplaced Identifier	Ser Phe Leu Ala Leu Gln Met Phe Ile Asp	
158	Unknown or Misplaced Identifier	50	55
159	Unknown or Misplaced Identifier	TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG	
160	Unknown or Misplaced Identifier	Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg	
161	Unknown or Misplaced Identifier	65	70
162	Unknown or Misplaced Identifier	TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT	
163	Unknown or Misplaced Identifier	Ser Val Asp Glu Asp Glu Asp Asp Glu Asp	
164	Unknown or Misplaced Identifier	85	90
165	Unknown or Misplaced Identifier	GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC	
166	Unknown or Misplaced Identifier	Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe	
167	Unknown or Misplaced Identifier	100	105
168	Unknown or Misplaced Identifier	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT	
169	Unknown or Misplaced Identifier	Glu Glu Glu Glu Leu Glu Asn Leu Met Asp	
170	Unknown or Misplaced Identifier	115	120
171	Unknown or Misplaced Identifier	GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT	
172	Unknown or Misplaced Identifier	Ala Glu Glu Glu Met Ser Val Glu Met Gly	
173	Unknown or Misplaced Identifier	130	135
174	Unknown or Misplaced Identifier	GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	
175	Unknown or Misplaced Identifier	Gly Ala Gly Ala Asn Cys Ala Cys Val Pro	
176	Unknown or Misplaced Identifier	145	150
177	Unknown or Misplaced Identifier	AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC	
178	Unknown or Misplaced Identifier	Asn Glu Val Lys Cys Arg Met Ile Tyr Phe	
179	Unknown or Misplaced Identifier	165	170
180	Unknown or Misplaced Identifier	CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA	
181	Unknown or Misplaced Identifier	Leu Val Ser Ile Pro Val Asn Pro Lys Glu	
182	Unknown or Misplaced Identifier	180	185
183	Unknown or Misplaced Identifier	GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA	
184	Unknown or Misplaced Identifier	Glu Asn Ala Asp Glu Glu Val Ala Met Glu	
185	Unknown or Misplaced Identifier	195	200 210
186	Unknown or Misplaced Identifier	GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC	
187	Unknown or Misplaced Identifier	Glu Glu Glu Glu Glu Glu Glu Met Gly Asn	
188	Unknown or Misplaced Identifier	220	225
190	Unknown or Misplaced Identifier	TAG	
191	Unknown or Misplaced Identifier	(2)A	
193	Unknown or Misplaced Identifier	A	
195	Unknown or Misplaced Identifier	A	
198	Unknown or Misplaced Identifier	A	
201	Unknown or Misplaced Identifier	A	
204	Unknown or Misplaced Identifier	A	
206	Unknown or Misplaced Identifier	A	
212	Unknown or Misplaced Identifier	GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACA	
213	Unknown or Misplaced Identifier	TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAG	
214	Unknown or Misplaced Identifier	TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTG	

LINE ERROR

ORIGINAL TEXT

215	Unknown or Misplaced Identifier	ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTT
218	Unknown or Misplaced Identifier	T
219	Unknown or Misplaced Identifier	(2)A
221	Unknown or Misplaced Identifier	A
223	Unknown or Misplaced Identifier	A
226	Unknown or Misplaced Identifier	A
229	Unknown or Misplaced Identifier	A
232	Unknown or Misplaced Identifier	A
234	Unknown or Misplaced Identifier	A
240	Unknown or Misplaced Identifier	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAG
241	Unknown or Misplaced Identifier	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGC
242	Unknown or Misplaced Identifier	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTG
243	Unknown or Misplaced Identifier	AAGTTTTGCA AGTTCGCCT ACAGCTCTAG CTTGTGA
244	Unknown or Misplaced Identifier	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCC
245	Unknown or Misplaced Identifier	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAG
246	Unknown or Misplaced Identifier	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCC
247	Unknown or Misplaced Identifier	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCG
248	Unknown or Misplaced Identifier	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCG
249	Unknown or Misplaced Identifier	ACCTTTGTG CC A
250	Unknown or Misplaced Identifier	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC
251	Unknown or Misplaced Identifier	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT
252	Unknown or Misplaced Identifier	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA
253	Unknown or Misplaced Identifier	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG
254	Unknown or Misplaced Identifier	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA
255	Unknown or Misplaced Identifier	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC
256	Unknown or Misplaced Identifier	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC
257	Unknown or Misplaced Identifier	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT
258	Unknown or Misplaced Identifier	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT
259	Unknown or Misplaced Identifier	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA
260	Unknown or Misplaced Identifier	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT
261	Unknown or Misplaced Identifier	GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG
262	Unknown or Misplaced Identifier	TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG
263	Unknown or Misplaced Identifier	AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT
264	Unknown or Misplaced Identifier	GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA
265	Unknown or Misplaced Identifier	GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT
266	Unknown or Misplaced Identifier	TAG A
268	Unknown or Misplaced Identifier	GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACA
269	Unknown or Misplaced Identifier	TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTT
270	Unknown or Misplaced Identifier	ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGT
271	Unknown or Misplaced Identifier	CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGAT
272	Unknown or Misplaced Identifier	GTTAAAAATA AAAGTTTGAC TTGCATAC A
275	Unknown or Misplaced Identifier	T
276	Unknown or Misplaced Identifier	(2)A
278	Unknown or Misplaced Identifier	A
280	Unknown or Misplaced Identifier	A
283	Unknown or Misplaced Identifier	A
286	Unknown or Misplaced Identifier	A
289	Unknown or Misplaced Identifier	A
291	Unknown or Misplaced Identifier	A
296	Unknown or Misplaced Identifier	ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAG
297	Unknown or Misplaced Identifier	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGC
298	Unknown or Misplaced Identifier	CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTG
299	Unknown or Misplaced Identifier	AAGTTTTGCA AGTTCGCCT ACAGCTCTAG CTTGTGA

LINE ERROR

ORIGINAL TEXT

300	Unknown or Misplaced Identifier	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCC
301	Unknown or Misplaced Identifier	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAG
302	Unknown or Misplaced Identifier	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCC
303	Unknown or Misplaced Identifier	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCG
304	Unknown or Misplaced Identifier	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCG
305	Unknown or Misplaced Identifier	ACCCTTTGTG CC A
306	Unknown or Misplaced Identifier	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC
307	Unknown or Misplaced Identifier	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT
308	Unknown or Misplaced Identifier	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA
309	Unknown or Misplaced Identifier	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG
310	Unknown or Misplaced Identifier	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA
311	Unknown or Misplaced Identifier	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC
312	Unknown or Misplaced Identifier	GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC
313	Unknown or Misplaced Identifier	GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT
314	Unknown or Misplaced Identifier	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT
315	Unknown or Misplaced Identifier	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA
316	Unknown or Misplaced Identifier	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT
317	Unknown or Misplaced Identifier	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGG
318	Unknown or Misplaced Identifier	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGT
319	Unknown or Misplaced Identifier	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCC
320	Unknown or Misplaced Identifier	CCCCACTCCT TGCTCCGCTC TCTTTCTTT TCCCACC
321	Unknown or Misplaced Identifier	TTCACTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCT
322	Unknown or Misplaced Identifier	TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCT
323	Unknown or Misplaced Identifier	TTCAAGCTTC CCCATTTGCT CCTCTCCCGA AACCTCT
324	Unknown or Misplaced Identifier	CCTTTTCGCG CTTTTTCTTT CTTGCTCCCC TCCCCCT
325	Unknown or Misplaced Identifier	TCACCAGCTT TGCTCTCCCT GCTCCCCCTC CCCTTTT
326	Unknown or Misplaced Identifier	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTT
327	Unknown or Misplaced Identifier	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTAT
328	Unknown or Misplaced Identifier	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGC
329	Unknown or Misplaced Identifier	CCTCCCTCCC CCTCCCCAGG CTTTTTTTTT TTTTTTT
330	Unknown or Misplaced Identifier	TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTG
331	Unknown or Misplaced Identifier	TCACCTCTGA GACCAGGCTG GCCTCAAAC CAGAAAT
332	Unknown or Misplaced Identifier	CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGAC
333	Unknown or Misplaced Identifier	GCCTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCC
334	Unknown or Misplaced Identifier	AACTCCCCCT TTGGCACCTT TCCTTTACAG GACCCCC
335	Unknown or Misplaced Identifier	TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCC
336	Unknown or Misplaced Identifier	CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCT
337	Unknown or Misplaced Identifier	GCCCCGTTCC CTTTTTTTGT GCCTTTCCTC CTGGCTC
338	Unknown or Misplaced Identifier	T
340	Unknown or Misplaced Identifier	AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTT
341	Unknown or Misplaced Identifier	TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCC
342	Unknown or Misplaced Identifier	CCTCTGTGTG CTTTTCTGT TCCCTCCCCC TCGCTGG
343	Unknown or Misplaced Identifier	TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACC
344	Unknown or Misplaced Identifier	CTTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCT
345	Unknown or Misplaced Identifier	CCTGACCCTG CTCCCCCTCC CCTCCCAGCT CCCCCCT
346	Unknown or Misplaced Identifier	CCTTCTCTCA GCCTGTCAAC CCTCCTTCTC TCCTCTC
347	Unknown or Misplaced Identifier	TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCC
348	Unknown or Misplaced Identifier	GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTG
349	Unknown or Misplaced Identifier	CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCT
350	Unknown or Misplaced Identifier	ATGTGTCTCT CTTCTATCT ATCCCTTCTT TTCTGTC
351	Unknown or Misplaced Identifier	CCATCACCTC TCTCCTCCCT TCCCTTCTCT CTCTCTT
352	Unknown or Misplaced Identifier	CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTA
353	Unknown or Misplaced Identifier	TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTC

LINE ERROR

ORIGINAL TEXT

354	Unknown or Misplaced Identifier	ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTC
355	Unknown or Misplaced Identifier	TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTT
356	Unknown or Misplaced Identifier	TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCC
357	Unknown or Misplaced Identifier	CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGA
358	Unknown or Misplaced Identifier	ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCC
359	Unknown or Misplaced Identifier	AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAG
360	Unknown or Misplaced Identifier	AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAG
361	Unknown or Misplaced Identifier	CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACA
362	Unknown or Misplaced Identifier	CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGG
363	Unknown or Misplaced Identifier	GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGG
364	Unknown or Misplaced Identifier	TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGAT
365	Unknown or Misplaced Identifier	TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTAT
366	Unknown or Misplaced Identifier	GGCTAAAGAT	ACTTGGAAAC	ATAGAAGCGT	TGTTAAA
367	Unknown or Misplaced Identifier	TTGCTAAAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCC
368	Unknown or Misplaced Identifier	GT GTT CCT	GGC CAT CAT	TTA AGG AAG	AAT G
369	Unknown or Misplaced Identifier	AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT
370	Unknown or Misplaced Identifier	ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG
371	Unknown or Misplaced Identifier	AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG
372	Unknown or Misplaced Identifier	GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA
373	Unknown or Misplaced Identifier	TTC TCA CCT	TAG A		
374	Unknown or Misplaced Identifier	GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCTTA
375	Unknown or Misplaced Identifier	GCTAAGAGCA	TCTTTTTTAAA	AAATATTATT	GGTAAAC
376	Unknown or Misplaced Identifier	TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTAT
377	Unknown or Misplaced Identifier	CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCC
378	Unknown or Misplaced Identifier	GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAG
379	Unknown or Misplaced Identifier	GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGG
380	Unknown or Misplaced Identifier	TTCTTATAGT	ACCTTTTGAGA	CAGCTGATAA	CAGCTGA
381	Unknown or Misplaced Identifier	TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAAT
382	Unknown or Misplaced Identifier	TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAA
383	Unknown or Misplaced Identifier	CTTAAATTTT	CCTTCATCTT	TAATTTTCCT	TAACTTT
384	Unknown or Misplaced Identifier	TAGAATTCAA	TTCAAATTCT	TAATTCATC	TTAATTT
385	Unknown or Misplaced Identifier	AATGTTTTTT	AAAAAAAATG	CAAATCTCAT	TTTTAAG
386	Unknown or Misplaced Identifier	GTAAC TG GGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGT
387	Unknown or Misplaced Identifier	GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAA
388	Unknown or Misplaced Identifier	CAGTAGGTTA	GTGAGGTGTA	TATGATCAGA	TTATGGA
389	Unknown or Misplaced Identifier	ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAAC
390	Unknown or Misplaced Identifier	ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATA
392	Unknown or Misplaced Identifier	AGTCAGGAGT	GTATTCTAAT	AAGTGTGCT	TATCTCT
393	Unknown or Misplaced Identifier	AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAA
394	Unknown or Misplaced Identifier	TTTTTTCCCC	TTCATTAATT	TTCTAGTTTT	TAGTAAT
395	Unknown or Misplaced Identifier	TTTTGTTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAA
396	Unknown or Misplaced Identifier	GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACT
397	Unknown or Misplaced Identifier	AATAAAAGTT	TGACTTGCAT	AC A	
399	Unknown or Misplaced Identifier	T			
400	Unknown or Misplaced Identifier	(2)A			
402	Unknown or Misplaced Identifier	A			
404	Unknown or Misplaced Identifier	A			
407	Unknown or Misplaced Identifier	A			
410	Unknown or Misplaced Identifier	A			
413	Unknown or Misplaced Identifier	A			
415	Unknown or Misplaced Identifier	A			
419	Unknown or Misplaced Identifier	Leu Leu His Arg Tyr Ser Leu Glu Glu Ile			
420	Unknown or Misplaced Identifier	5			10

LINE ERROR

ORIGINAL TEXT

421	Unknown or Misplaced Identifier	Val Phe Ala Val Val Thr Thr Ser Phe
422	Unknown or Misplaced Identifier	20
423	Unknown or Misplaced Identifier	T
425	Unknown or Misplaced Identifier	(2)A
427	Unknown or Misplaced Identifier	A
429	Unknown or Misplaced Identifier	A
432	Unknown or Misplaced Identifier	A
435	Unknown or Misplaced Identifier	A
438	Unknown or Misplaced Identifier	A
440	Unknown or Misplaced Identifier	A
446	Unknown or Misplaced Identifier	GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTG
447	Unknown or Misplaced Identifier	GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGA
448	Unknown or Misplaced Identifier	TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGG
449	Unknown or Misplaced Identifier	GGCCCGTGGG TTCCTCTTCC TGGAGCTCCA GGAACCA
450	Unknown or Misplaced Identifier	TGGTCTGAGA CAGTATCCTC AGGTACACAGA GCAGAGG
451	Unknown or Misplaced Identifier	GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGG
452	Unknown or Misplaced Identifier	CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCT
453	Unknown or Misplaced Identifier	CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTG
454	Unknown or Misplaced Identifier	TTCCTCCTTC AGGTTTTTCAG GGGACAGGCC AACCCAG
455	Unknown or Misplaced Identifier	CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGT
456	Unknown or Misplaced Identifier	TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTC
457	Unknown or Misplaced Identifier	CTCTCCCCAG GCCTGTGGGT CTTCAATTGCC CAGCTCC
458	Unknown or Misplaced Identifier	GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAG
459	Unknown or Misplaced Identifier	ACTGCAAGCC TGAGGAAGCC CTTGAGGCC AACCAAG
460	Unknown or Misplaced Identifier	GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTC
461	Unknown or Misplaced Identifier	CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCT
462	Unknown or Misplaced Identifier	AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCAC
463	Unknown or Misplaced Identifier	CCCACTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGC
464	Unknown or Misplaced Identifier	TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAG
465	Unknown or Misplaced Identifier	TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGA
466	Unknown or Misplaced Identifier	GCAGAAATGC TGGAGAGTGT CATCAAAAT TACAAGC
467	Unknown or Misplaced Identifier	GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTC
468	Unknown or Misplaced Identifier	TGAAGGAAGC AGACCCACC GGCCACTCCT ATGTCCT
469	Unknown or Misplaced Identifier	GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGA
470	Unknown or Misplaced Identifier	AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATG
471	Unknown or Misplaced Identifier	CTCCTGAGGA GGAATCTGG GAGGAGCTGA GTGTGAT
472	Unknown or Misplaced Identifier	GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGC
473	Unknown or Misplaced Identifier	TTTGGTGCA GAAAAGTACC TGGAGTACGG CAGGTGC
474	Unknown or Misplaced Identifier	CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTC
475	Unknown or Misplaced Identifier	ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGC
476	Unknown or Misplaced Identifier	TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGG
477	Unknown or Misplaced Identifier	CTGAGCATGA GTTGACAGCA AGGCCAGTGG GAGGGGG
478	Unknown or Misplaced Identifier	ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTC
479	Unknown or Misplaced Identifier	CCCATCTTTC ACTCTGAAGA GAGCGGTCAG TGTTCTC
480	Unknown or Misplaced Identifier	TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCT
481	Unknown or Misplaced Identifier	TCAAATGTTT TTTTATAAGG GATGGTTGAA TGAACCT
482	Unknown or Misplaced Identifier	TATGAATGAC AGCAGTCACA CAGTTCCTGT TATATAG
483	Unknown or Misplaced Identifier	GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTAT
484	Unknown or Misplaced Identifier	ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGA
485	Unknown or Misplaced Identifier	AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGAT
486	Unknown or Misplaced Identifier	CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGAT
488	Unknown or Misplaced Identifier	GATTTCCCTG GCTTCTTTGA GAATGTAAGA GAAATTA
489	Unknown or Misplaced Identifier	AATTCCTCCT GTTCACTGGC TCTTTTCTTC TCCATGC

LINE ERROR

ORIGINAL TEXT

490	Unknown or Misplaced Identifier	TTTTTGGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAA
491	Unknown or Misplaced Identifier	CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGC
492	Unknown or Misplaced Identifier	AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGT
493	Unknown or Misplaced Identifier	GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGG	GTGTCAA
494	Unknown or Misplaced Identifier	GGCATTITGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGG
495	Unknown or Misplaced Identifier	AATGATCTTG	GGTGGATCC	A	
495	Unknown or Misplaced Identifier	AATGATCTTG	GGTGGATCC	A	

Felfe and Lynch
805 Third Avenue
New York, NY 10022

Thierry Boon
07/28/838
July 9, 1991

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Mailed: 9/19/91

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with one or more of the requirements of 37 CFR §§ 1.821 through 1.825 as follows:

- ☐ 1. This application clearly fails to comply with the collective requirements of §§ 1.821 through 1.825. Applicant's attention is directed to these regulations, a copy of which is attached.
- ☐ 2. This application does not conform exclusively to the requirements of §§ 1.821 through 1.825. The non-conforming material should be deleted. § 1.821(b).
- ☐ 3. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." § 1.821(c).
- ☐ 4. This application does contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." However, the "Sequence Listing" does not comply with the requirements of §§ 1.821 through 1.825 as follows:
 - ☐ a. The sequence data does not comply with the symbol and format requirements of paragraphs (b) through (p) of § 1.822. Specifically: _____
 - ☐ b. The "Sequence Listing" does not comply with the location and page requirements of paragraph (a) of § 1.823.
 - ☐ c. The "Sequence Listing" does not comply with the information requirements of paragraph (b) of § 1.823. Specifically: _____
 - ☐ d. Other: _____
- ☐ 5. The description and/or claims of the patent application mention a sequence that is set forth in the "Sequence Listing" but reference is not properly made to the sequence by use of a sequence identifier as required by § 1.821(d).
- ☐ 6. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by § 1.821(e).
- ☐ 7. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the computer readable form does not comply with the requirements of § 1.824. Specifically: _____
- ☐ 8. A statement that the content of the paper and computer readable copies are the same has not been submitted as required by § 1.821(f).
- ☒ 9. The amendment to or replacement of the paper and/or computer readable copies of the "Sequence Listing" does not comply with the requirements of § 1.825(a) through (c).
- ☐ 10. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically: _____
- ☐ 11. Other: _____

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE ABOVE REQUIREMENTS. Failure to comply with the above requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR § 1.136. Direct the response to, and any questions about, this notice to the undersigned. A copy of this notice MUST be returned with your response.



For: Manager, Application Processing Division



Examining Group _____

Felfe and Lynch
805 Third Avenue
New York, NY 10022

Thierry Boon
07/728,838
July 9, 1991

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Mailed: 10/01/91

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). However, this application fails to comply with one or more of the requirements of 37 CFR §§ 1.821 through 1.825 as follows:

- ☐ 1. This application clearly fails to comply with the collective requirements of §§ 1.821 through 1.825. Applicant's attention is directed to these regulations, a copy of which is attached.
- ☐ 2. This application does not conform exclusively to the requirements of §§ 1.821 through 1.825. The non-conforming material should be deleted. § 1.821(b).
- ☐ 3. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." § 1.821(c).
- ☐ 4. This application does contain, as a separate part of the disclosure on paper copy, a "Sequence Listing." However, the "Sequence Listing" does not comply with the requirements of §§ 1.821 through 1.825 as follows:
 - ☐ a. The sequence data does not comply with the symbol and format requirements of paragraphs (b) through (p) of § 1.822. Specifically: _____
 - ☐ b. The "Sequence Listing" does not comply with the location and page requirements of paragraph (a) of § 1.823.
 - ☐ c. The "Sequence Listing" does not comply with the information requirements of paragraph (b) of § 1.823. Specifically: _____
 - ☐ d. Other: _____
- ☐ 5. The description and/or claims of the patent application mention a sequence that is set forth in the "Sequence Listing" but reference is not properly made to the sequence by use of a sequence identifier as required by § 1.821(d).
- ☐ 6. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by § 1.821(e).
- ☒ 7. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the computer readable form does not comply with the requirements of § 1.824. Specifically: the information is not in ASCII format
- ☒ 8. A statement that the content of the paper and computer readable copies are the same has not been submitted as required by § 1.821(f).
- ☒ 9. The amendment to or replacement of the paper and/or computer readable copies of the "Sequence Listing" does not comply with the requirements of § 1.825(a) through (c).
- ☐ 10. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable. Applicant must provide a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. § 1.825(d). Specifically: _____
- ☐ 11. Other: _____

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE ABOVE REQUIREMENTS. Failure to comply with the above requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR § 1.136. Direct the response to, and any questions about, this notice to the undersigned. A copy of this notice MUST be returned with your response.

☒ C. Barnas
For: Manager, Application Processing Division
(703) 308-1202 or 308-1203

☐ _____
Examining Group _____
(703) 308- _____